GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 28, 2003, 12:02:57 ; Search time 114.384 Seconds
(without alignments)
880.694 Million cell updates/sec

Title: US-09-924-946-2
Perfect score: 4180
Sequence: 1 MAWSPPATLFLFLLLLGQPP.....YPANAELSLEQEQRLRNNLI 756

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4180	100.0	756	23	AAE19380	Human endothelial
2	4174	99.9	756	23	AAM48743	Human 47765 lysyl
3	4170	99.8	756	23	AAE21043	Human drug metabol
4	4085.5	97.7	743	23	AAG66060	Human lysyl oxidas
5	3645.5	87.2	757	21	AAB19127	Polypeptide isolat
6	3641.5	87.1	757	23	ABB07650	Human lysyl-oxidas
7	3047.5	72.9	573	21	AAB49534	Clone HOHEC84 #1.
8	2278.5	54.5	769	22	AAE11940	Human lipid metabo
9	2268.5	54.3	774	21	AAB00077	Human lysyl oxidas
10	2268.5	54.3	774	23	ABB07649	Human LOR-1 protei
11	2263	54.1	752	23	ABB07653	Human lysyl-oxidas
12	2263	54.1	753	21	AAB00073	Human lysyl oxidas
13	2263	54.1	753	22	AAG65903	Amino acid sequenc
14	2263	54.1	753	23	AAE15549	Human secreted pro
15	2263	54.1	753	23	AAG66059	Human lysyl oxidas
16	2249	53.8	753	22	AAE11935	Human CG153 (or C5
17	2232	53.4	443	21	AAY72125	Peptide fragment #
18	2232	53.4	443	21	AAB49549	Protein fragment:
19	2223	53.2	408	21	AAB51785	Human secreted pro
20	2222	53.2	754	21	AAB00078	Murine lysyl oxida
21	2163.5	51.8	732	22	AAE11927	Human CG153 (or C5
22	1890.5	45.2	608	22	AAE11936	Human CG153 (or C5
23	1832	43.8	638	23	AAG66058	Human lysyl oxidas
24	1773	42.4	641	21	AAB12307	Human secreted pro
25	1282	30.7	227	23	AAE19385	Human endothelial
26	1138	27.2	298	23	AAU76451	Human lysyloxidase
27	1122	26.8	396	21	AAB51784	Gene 15 human secr
28	939.5	22.5	511	22	ABB60618	Drosophila melanog
29	833	19.9	171	21	AAB49538	Clone HOHEC84 #2.
30	833	19.9	171	21	AAB51741	Human secreted pro
31	751	18.0	1785	19	AAW64591	Human SRCR protein
32	694	16.6	125	23	AAE19382	Human endothelial
33	682	16.3	552	22	AAE09447	Human sbg14862SPER
34	655.5	15.7	1436	22	AAB66088	Bovine WC1 protein
35	633.5	15.2	822	20	AAW99087	Human serine prote
36	633.5	15.2	875	20	AAW83361	Human neurotrypsin
37	628	15.0	1116	23	AAU97582	Human CD163 recept
38	626	15.0	1121	22	AAM39493	Human polypeptide
39	626	15.0	1124	22	AAM41279	Human polypeptide
40	626	15.0	1124	22	AAM41280	Human polypeptide
41	626	15.0	1151	23	AAU97585	Human CD163 recept
42	626	15.0	1156	23	AAU97584	Human CD163 recept
43	624	14.9	360	22	ABB58607	Drosophila melanog
44	622.5	14.9	422	22	AAE09446	Human sbg14862SPER
45	619.5	14.8	1149	23	AAU97583	Human CD163 recept

ALIGNMENTS

RESULT 1
AAE19380
ID AAE19380 standard; Protein; 756 AA.
XX
AC AAE19380;
XX
DT 31-MAY-2002 (first entry)
XX
DE Human endothelial estrogen regulated (EER)-7 protein.
XX
KW Human; lysyl oxidase; LO protein; endothelial estrogen regulated protein;
KW AAA; abdominal aortic aneurysms; EER-7 protein; myocardial infraction;
KW elastin; fibrotic disease; gene therapy; cardiant.
XX
OS Homo sapiens.
XX
PN WO200212470-A2.
XX
PD 14-FEB-2002.
XX
PF 08-AUG-2001; 2001WO-US24942.
XX
PR 08-AUG-2000; 2000US-223763P.
PR 15-DEC-2000; 2000US-255838P.
XX
PA (AMHP) AMERICAN HOME PROD CORP.
XX
PI Evans MJ, Scicchitano MS, Bapat AR, Beer E, Bhat RA, Ferris E;
PI Mastroeni R, Zhang J, Karathanasis SK;
XX
DR WPI; 2002-227150/28.
DR N-PSDB; AAD30517.
XX

PT Novel isolated endothelial estrogen regulated gene protein comprising
PT lysyl oxidase activity and conserved catalytic domain of lysyl oxidase,
PT useful as target to treat abdominal aortic aneurysms, myocardial
PT infarction -
XX
PS Claim 1; Page 63-64; 68pp; English.
XX
CC The patent discloses novel lysyl oxidase (LO) genes, termed endothelial
CC estrogen regulated (EER)-7 genes and their corresponding proteins. The
CC invention also relates to an assay system to identify compounds that
CC selectively modulate EER7 protein activity by interaction with estrogen
CC receptors. Stimulation of LO enzyme activity of EER-7 acts as a target
CC for abdominal aortic aneurysms (AAA) and myocardial infractions. Increase
CC in EER-7 lysyl oxidase activity increases elastin cross-linking in the
CC inner elastic lamina which prevents development of aneurysms. Increased
CC EER-7 is also useful to increase collagen cross-linkings which increase
CC tensile strength of vessel wall which also prevents aneurysms. Myocardial
CC infraction is prevented by inhibiting rupture of fibrous cap that covers
CC plaque in the coronary vessels. Increased tensile strength of the cap,
CC resulting from increased LO activity helps preventing the infractions.
CC Inhibition of LO activity is useful for treating fibrotic diseases.
CC Stimulation of EER-7 proteins are useful for treating patients with
CC estrogen-related disease states. Genetic variants of EER-7 can be
CC detected to diagnose an EER-7 associated disease such as AAA or
CC myocardial infarction. EER-7 polynucleotides are useful in gene
CC therapy. The present sequence is human EER-7 protein.
XX
SQ Sequence 756 AA;

Query Match 100.0%; Score 4180; DB 23; Length 756;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 756; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MAWSPPATLFLFLLLLGQPPPSRPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWGTVCDD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAWSPPATLFLFLLLLGQPPPSRPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWGTVCDD 60

Qy      61 NFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSNGWGVS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 NFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSNGWGVS 120

Qy     121 DCSHSEDVGVICHPRRHRGYLSETVSNALGPQGRRLEEVRLKPILASAKQHSPVTEGAVE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DCSHSEDVGVICHPRRHRGYLSETVSNALGPQGRRLEEVRLKPILASAKQHSPVTEGAVE 180

Qy     181 VKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRKVWDLKMRDPKSRLKSLTN 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 VKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRKVWDLKMRDPKSRLKSLTN 240

Qy     241 KNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHAVVSCVAGPHFRPPKTKPQ 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 KNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHAVVSCVAGPHFRPPKTKPQ 300

Qy     301 RKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVVCRQLGFGSAREA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 RKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVVCRQLGFGSAREA 360

Qy     361 LFGARLGQGLGPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENAAAVRCNVPNMGFQNQ 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 LFGARLGQGLGPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENAAAVRCNVPNMGFQNQ 420

Qy     421 VRLAGGRIPEEGLLEVQVEVNGVPRWGSVCSENWGLTEAMVACRQLGLGFAIHAYKETWF 480
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Db     421 VRLAGGRIPEEGLLEVQVEVNGVPRWGSVCSENWGLTEAMVACRQLGLGFAIHAYKETWF 480

Qy     481 WSGTPRAQEVVMSGVRCSGTELALQQCQRHGPVHCSHGGGRFLAGVSCMDSAPDLVMNAQ 540
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Db     481 WSGTPRAQEVVMSGVRCSGTELALQQCQRHGPVHCSHGGGRFLAGVSCMDSAPDLVMNAQ 540

Qy     541 LVQETAYLEDRPLSQLYCAHEENCLSKSADHMDWPYGYRRLLRFSTQIYNLGRTDFRPKT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 LVQETAYLEDRPLSQLYCAHEENCLSKSADHMDWPYGYRRLLRFSTQIYNLGRTDFRPKT 600
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Qy     601 GRDSWVWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKAS FCLEDTNCPTGLQRRYACAN 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GRDSWVWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKAS FCLEDTNCPTGLQRRYACAN 660

Qy     661 FGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIV PHYEVAESDFSNNMLQCRCK 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 FGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIV PHYEVAESDFSNNMLQCRCK 720

Qy     721 YDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI 756
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Db     721 YDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI 756
```

RESULT 2
AAM48743
ID AAM48743 standard; Protein; 756 AA.
XX
AC AAM48743;
XX
DT 02-APR-2002 (first entry)
XX
DE Human 47765 lysyl oxidase SEQ ID NO 2.
XX
KW Human; 47765; lysyl oxidase; LSO; cytostatic; haemostatic; hepatotropic;
KW cardiant; osteopathic; dermatological; antiarteriosclerotic; vasotropic;
KW antiinflammatory; hypotensive; antiarrhythmic; cell proliferation;
KW growth; differentiation; leukaemia; tumour; cancer; bone; cartilage;
KW myeloproliferative; muscular; osteoporosis; cardiovascular; gene therapy;
KW chromosome mapping; tissue typing; forensic; pharmacogenomic; enzyme.
XX
OS Homo sapiens.
XX
PN WO200192495-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001WO-US17405.
XX
PR 26-MAY-2000; 2000US-207650P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Meyers R;
XX
DR WPI; 2002-122067/16.
DR N-PSDB; ABA96419, ABA96420.
XX
PT Novel human lysyl oxidase polypeptide, designated 47765, and
PT polynucleotides, useful in the diagnosis and treatment of cell
PT proliferation disorders, muscular disorders, bone disorders and skin
PT elasticity disorders -
XX
PS Claim 14; Fig 1; 115pp; English.
XX
CC The invention relates to human lysyl oxidase (LSO) polypeptide,
CC designated 47765 with cytostatic, haemostatic, hepatotropic, cardiant,
CC osteopathic, dermatological, antiarteriosclerotic, vasotropic,
CC antiinflammatory, hypotensive and antiarrhythmic activity. 47765
CC molecules are useful for identifying a compound which modulates the
CC activity of the protein, for developing novel diagnostic and therapeutic
CC agents for LSO-mediated or related disorders including cell
CC proliferation, growth or differentiation disorder (e.g. carcinoma,
CC leukaemia, tumour angiogenesis, hepatic disorders and haematopoietic,
CC myeloproliferative disorders), muscular disorders (e.g. cardiac muscle
CC disorder, paralysis, ataxia, myotonia and myokymia), bone disorders (e.g.
CC osteochondrosis and osteoporosis), skin elasticity disorders (e.g. cutis
CC laxa, Ehlers-Danlos type V syndrome), cardiovascular disorders (e.g.
CC arteriosclerosis, ischaemia reperfusion injury, restenosis, arterial
CC inflammation, vascular wall remodeling, tachycardia, vascular heart
CC disease, long QT syndrome, congestive heart failure, hypertension,
CC coronary artery disease and arrhythmia) or cartilage based disorders
CC (e.g. chondromalacia and polychondritis). The encoding polynucleotide is
CC useful in chromosome mapping, tissue typing, forensic identification, as

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CC   markers for pharmacogenomic profiling of a subject and in gene therapy.
XX
SQ   Sequence   756 AA;

  Query Match             99.9%;  Score 4174;  DB 23;  Length 756;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  755;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MAWSPPATLFLFLLLLGQPPPSRPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWGTVCDD 60
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Db       1 MAWSPPATLFLFLLLLGQPPPSRPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWGTVCDD 60

Qy      61 NFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSNGWGVS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 NFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSNGWGVS 120

Qy     121 DCSHSEDVGVICHPRRHRGYLSETVSNALGPQGRRLEEVRLKPILASAKQHSPVTEGAVE 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DCSHSEDVGVICHPRRHRGYLSETVSNALGPQGRRLEEVRLKPILASAKQHSPVTEGAVE 180

Qy     181 VKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRKVWDLKMRDPKSRLKSLTN 240
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Db     181 VKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRKVWDLKMRDPKSRLKSLTN 240

Qy     241 KNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHAVVSCVAGPHFRPPKTKPQ 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 KNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHAVVSCVAGPHFRPPKTKPQ 300

Qy     301 RKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVVCRQLGFGSAREA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 RKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVVCRQLGFGSAREA 360

Qy     361 LFGARLGQGLGPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENAAAVRCNVPNMGFQNQ 420
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Db     361 LFGARLGQGLGPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENDAAVRCNVPNMGFQNQ 420

Qy     421 VRLAGGRIPEEGLLEVQVEVNGVPRWGSVCSENWGLTEAMVACRQLGLGFAIHAYKETWF 480
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Qy     481 WSGTPRAQEVVMSGVRCSGTELALQQCQRHGPVHCSHGGGRFLAGVSCMDSAPDLVMNAQ 540
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Db     481 WSGTPRAQEVVMSGVRCSGTELALQQCQRHGPVHCSHGGGRFLAGVSCMDSAPDLVMNAQ 540

Qy     541 LVQETAYLEDRPLSQLYCAHEENCLSKSADHMDWPYGYRRLLRFSTQIYNLGRTDFRPKT 600
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Db     541 LVQETAYLEDRPLSQLYCAHEENCLSKSADHMDWPYGYRRLLRFSTQIYNLGRTDFRPKT 600

Qy     601 GRDSWVWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTNCPTGLQRRYACAN 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GRDSWVWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTNCPTGLQRRYACAN 660

Qy     661 FGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAESDFSNNMLQCRCK 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 FGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAESDFSNNMLQCRCK 720

Qy     721 YDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI 756
           |||||||||||||||||||||||||||||||||||||
Db     721 YDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI 756


RESULT 3
AAE21043
ID   AAE21043 standard; Protein; 756 AA.
XX
AC   AAE21043;
XX
DT   01-JUL-2002  (first entry)
XX
DE   Human drug metabolising enzyme (DME-1) protein.
XX
KW   Human; drug metabolising enzyme; cell proliferative disorder; metabolic;
KW   autoimmune; inflammatory; developmental; gastrointestinal; hypergonadal;
KW   pancreatic; endocrine; eye; dermatitis; Addison's disease; antilipaemic;
KW   acquired immunodeficiency syndrome; AIDS; glomerulonephritis; anorectic;
KW   diabetes; atherosclerosis; adult respiratory distress syndrome; anaemia;
KW   Grave's disease; thyroiditis; Crohn's disease; infection; anticoagulant;
KW   systemic lupus erythematosus; cirrhosis; psoriasis; epilepsy; gastritis;
KW   cataract; hypopituitarism; cancer; rheumatoid arthritis; conjunctivitis;
KW   cystic fibrosis; peptic ulcer; Wilson's disease; hepatitis; antithyroid;
KW   allergy; diarrhoea; thrombosis; obesity; immunostimulant; tranquillizer;
KW   infertility; vulnerary; anticonvulsant; gynaecological; laxative; goitre;
KW   nootropic; jaundice; trauma; asthma; DME-1; enzyme.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..24
FT                   /label= Signal_peptide
FT   Protein         25..756
FT                   /note= "Mature human DME-1 protein"
FT   Domain          505..731
FT                   /note= "Copper domain"
XX
PN   WO200212467-A2.
XX
PD   14-FEB-2002.
XX
PF   03-AUG-2001; 2001WO-US24382.
XX
PR   04-AUG-2000; 2000US-223055P.
PR   11-AUG-2000; 2000US-224728P.
PR   18-AUG-2000; 2000US-226440P.
PR   24-AUG-2000; 2000US-228067P.
PR   31-AUG-2000; 2000US-230063P.
PR   13-SEP-2000; 2000US-232244P.
PR   20-SEP-2000; 2000US-234269P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Baughn MR,  Bruns CM,  Das D,  Delegeane AM,  Ding L,  Elliot VS;
PI   Gandhi AR,  Griffin JA,  Hafalia AJA,  Khan FA,  Lal P,  Lee S;
PI   Lu DAM,  Lu Y,  Patterson C,  Ramkumar J,  Ring HZ,  Sanjanwala MS;
PI   Tang YT,  Thangavelu K,  Thornton M,  Tribouley CM,  Walia NK;
PI   Warren BA,  Yang J,  Yao MG,  Yue H;
XX
DR   WPI; 2002-206331/26.
DR   N-PSDB; AAD33480.
XX
PT   New human drug metabolizing enzyme polypeptide and polynucleotide
PT   useful for diagnosing, treating and preventing cell proliferative,
PT   autoimmune/inflammatory, endocrine, eye, metabolic and gastrointestinal
PT   disorders  -
XX
PS   Claim 45; Page 144-146; 179pp; English.
XX
CC   The invention relates to an isolated human drug metabolising enzyme (DME)
CC   polypeptide or a biologically active or immunogenic fragment of DME. DME
CC   is useful for diagnosis, treatment and prevention of cell proliferative,
CC   autoimmune/inflammatory, developmental, endocrine, eye, metabolic and
CC   gastrointestinal disorders including live disorders. Autoimmune/
CC   inflammatory disorders include acquired immunodeficiency syndrome (AIDS),
CC   adult respiratory distress syndrome, Addison's disease, atherosclerosis,
CC   allergies, anaemia, asthma, autoimmune haemolytic anaemia, autoimmune
CC   thyroiditis, Crohn's disease, atopic dermatitis, diabetes mellitus,
CC   glomerulonephritis, rheumatoid arthritis, systemic lupus erythematosus,
CC   ulcerative colitis, uveitis, viral, bacterial, protozoal, parasitic,
CC   fungal, helminthic infections and trauma. Cell proliferative disorders
CC   include cancer, arteriosclerosis, cirrhosis and psoriasis; developmental
CC   disorders include epilepsy and cataract; and endocrine disorders include
CC   disorders of hypothalamus/pituitary, disorders associated with
CC   hypopituitarism, including diabetes insipidus, hypogonadism, disorders
CC   associated with hypothyroidism including goitre, Grave's disease,
CC   pancreatic disorders such as diabetes mellitus, disorders associated with
CC   adrenals, disorders associated with gonadal steroid hormones such as
CC   endometriosis, infertility, hypergonadal disorders and gynaecomastia.
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CC   Disorders of the eye include conjunctivitis and macular degeneration and
CC   metabolic disorders include diabetes, cystic fibrosis, obesity and
CC   hypocalcaemia. Gastrointestinal disorders include gastritis, peptic
CC   ulcer, hepatitis, constipation, diarrhoea, jaundice, Wilson's disease,
CC   thrombosis and hepatic tumours. DME gene is useful in gene therapy. The
CC   present sequence is human DME-1 protein.
XX
SQ   Sequence   756 AA;

  Query Match             99.8%;  Score 4170;  DB 23;  Length 756;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches  754;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MAWSPPATLFLFLLLLGQPPPSRPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWGTVCDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAWSPPATLFLFLLLLGQPPPSRPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWGTVCDD 60

Qy      61 NFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSNGWGVS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 NFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSNGWGVS 120

Qy     121 DCSHSEDVGVICHPRRHRGYLSETVSNALGPQGRRLEEVRLKPILASAKQHSPVTEGAVE 180
           ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db     121 DCSHSEDVGVICHPRRHRGYLSETVSNALGPQGQRLEEVRLKPILASAKQHSPVTEGAVE 180

Qy     181 VKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRKVWDLKMRDPKSRLKSLTN 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 VKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRKVWDLKMRDPKSRLKSLTN 240

Qy     241 KNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHAVVSCVAGPHFRPPKTKPQ 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 KNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHAVVSCVAGPHFRPPKTKPQ 300

Qy     301 RKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVVCRQLGFGSAREA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 RKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVVCRQLGFGSAREA 360

Qy     361 LFGARLGQGLGPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENAAAVRCNVPNMGFQNQ 420
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     361 LFGARLGQGLGPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENDAAVRCNVPNMGFQNQ 420

Qy     421 VRLAGGRIPEEGLLEVQVEVNGVPRWGSVCSENWGLTEAMVACRQLGLGFAIHAYKETWF 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 VRLAGGRIPEEGLLEVQVEVNGVPRWGSVCSENWGLTEAMVACRQLGLGFAIHAYKETWF 480

Qy     481 WSGTPRAQEVVMSGVRCSGTELALQQCQRHGPVHCSHGGGRFLAGVSCMDSAPDLVMNAQ 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 WSGTPRAQEVVMSGVRCSGTELALQQCQRHGPVHCSHGGGRFLAGVSCMDSAPDLVMNAQ 540

Qy     541 LVQETAYLEDRPLSQLYCAHEENCLSKSADHMDWPYGYRRLLRFSTQIYNLGRTDFRPKT 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 LVQETAYLEDRPLSQLYCAHEENCLSKSADHMDWPYGYRRLLRFSTQIYNLGRTDFRPKT 600

Qy     601 GRDSWVWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTNCPTGLQRRYACAN 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GRDSWVWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTNCPTGLQRRYACAN 660

Qy     661 FGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAESDFSNNMLQCRCK 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 FGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAESDFSNNMLQCRCK 720

Qy     721 YDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI 756
           |||||||||||||||||||||||||||||||||||||
Db     721 YDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI 756


RESULT 4
AAG66060
ID   AAG66060 standard; Protein; 743 AA.
XX
AC   AAG66060;
XX
DT   27-FEB-2002  (first entry)
XX
DE   Human lysyl oxidase-like (LOXL4) protein.
XX
KW   Lysyl oxidase; lysyl oxidase-like; LOXL; LOX; neuroprotective; nootropic;
KW   dermatological; hepatotropic; cytostatic; antidote; LOXL4.
XX
OS   Homo sapiens.
XX
PN   WO200183702-A2.
XX
PD   08-NOV-2001.
XX
PF   03-MAY-2001; 2001WO-US14472.
XX
PR   03-MAY-2000; 2000US-201587P.
XX
PA   (UYHA-) UNIV HAWAII.
XX
PI   Csiszar K,  Boyd CD,  Kim Y,  Le Saux CJ,  Fong SFT;
XX
DR   WPI; 2002-041491/05.
DR   N-PSDB; AAI67789.
XX
PT   Novel copper-dependent lysyl oxidase-like proteins, nucleic acids
PT   encoding the protein for diagnostic assays aid identifying modulators
PT   useful for treating cancer, skin, copper-related, pulmonary or hepatic
PT   disorders -
XX
PS   Claim 5; Page 79-80; 82pp; English.
XX
CC   The invention provides lysyl oxidase-like (LOXL) polypeptides and
CC   polynucleotides encoding them. The LOXL proteins (LOXL3 and LOXL4) can be
CC   expressed by standard recombinant methodology. The LOXL polypeptides are
CC   useful for identifying their modulators which can be used for treating a
CC   disorder associated with LOX or LOXL polypeptide activity, including
CC   disorders related to extracellular matrix materials, a cell migration,
CC   cell proliferative disorder, skin, vascular system, developmental,
CC   skeletal, neurological, hepatic system, copper-related, pulmonary system
CC   disorders or lathyrism disorder and cancer in a subject. The LOXL
CC   polynucleotides are useful as probes and primers. The LOXL polypeptides
CC   are useful in bioassays, for the production of antibodies, useful for
CC   diagnostic assays to determine expression levels and localization of
CC   LOXL3 and LOXL4 proteins and other proteins of the LOX gene family in
CC   various tissue samples from healthy or infirm subjects and to purify the
CC   proteins. The antibodies are therapeutically useful to counteract or
CC   supplement the biological effect of LOXL proteins in vivo. The present
CC   sequence represents a human-derived LOXL4 protein.
XX
SQ   Sequence   743 AA;

  Query Match             97.7%;  Score 4085.5;  DB 23;  Length 743;
  Best Local Similarity   98.1%;  Pred. No. 0;
  Matches  742;  Conservative    0;  Mismatches    1;  Indels   13;  Gaps    1;

Qy       1 MAWSPPATLFLFLLLLGQPPPSRPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWGTVCDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAWSPPATLFLFLLLLGQPPPSRPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWGTVCDD 60

Qy      61 NFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSNGWGVS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 NFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSNGWGVS 120

Qy     121 DCSHSEDVGVICHPRRHRGYLSETVSNALGPQGRRLEEVRLKPILASAKQHSPVTEGAVE 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DCSHSEDVGVICHPRRHRGYLSETVSNALGPQGRRLEEVRLKPILASAKQHSPVTEGAVE 180

Qy     181 VKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRKVWDLKMRDPKSRLKSLTN 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 VKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYY-------------RLKSLTN 227

Qy     241 KNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHAVVSCVAGPHFRPPKTKPQ 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     228 KNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHAVVSCVAGPHFRPPKTKPQ 287
```

```
Qy     301 RKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVVCRQLGFGSAREA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     288 RKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVVCRQLGFGSAREA 347

Qy     361 LFGARLGQGLGPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENAAAVRCNVPNMGFQNQ 420
           ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     348 LFGARLGQGLGPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENDAAVRCNVPNMGFQNQ 407

Qy     421 VRLAGGRIPEEGLLEVQVEVNGVPRWGSVCSENWGLTEAMVACRQLGLGFAIHAYKETWF 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     408 VRLAGGRIPEEGLLEVQVEVNGVPRWGSVCSENWGLTEAMVACRQLGLGFAIHAYKETWF 467

Qy     481 WSGTPRAQEVVMSGVRCSGTELALQQCQRHGPVHCSHGGGRFLAGVSCMDSAPDLVMNAQ 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     468 WSGTPRAQEVVMSGVRCSGTELALQQCQRHGPVHCSHGGGRFLAGVSCMDSAPDLVMNAQ 527

Qy     541 LVQETAYLEDRPLSQLYCAHEENCLSKSADHMDWPYGYRRLLRFSTQIYNLGRTDFRPKT 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     528 LVQETAYLEDRPLSQLYCAHEENCLSKSADHMDWPYGYRRLLRFSTQIYNLGRTDFRPKT 587

Qy     601 GRDSWVWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTNCPTGLQRRYACAN 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     588 GRDSWVWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTNCPTGLQRRYACAN 647

Qy     661 FGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAESDFSNNMLQCRCK 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     648 FGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAESDFSNNMLQCRCK 707

Qy     721 YDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI 756
           ||||||||||||||||||||||||||||||||||||
Db     708 YDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI 743
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RESULT 5
AAB19127
ID AAB19127 standard; Protein; 757 AA.
XX
AC AAB19127;
XX
DT 19-FEB-2001 (first entry)
XX
DE Polypeptide isolated from lymph node stromal cells of fsn -/- mice.
XX
KW Lymph node stromal cell; fsn -/- mice; inflammatory disorder;
KW immune system disorder; cancer; viral disorder; HIV infection;
KW blood vessel growth; tumour necrosis factor disorder; arthritis;
KW inflammatory bowel disease; fibroblast growth factor-mediated disorder;
KW cardiac failure.
XX
OS Mus sp.
XX
PN WO200058463-A1.
XX
PD 05-OCT-2000.
XX
PF 18-FEB-2000; 2000WO-NZ00015.
XX
PR 25-MAR-1999; 99US-0276268.
PR 26-AUG-1999; 99US-0383586.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Strachan L, Sleeman M, Abernethy N, Onrust R, Kumble KD;
PI Murison JG;
XX
DR WPI; 2000-664924/64.
DR N-PSDB; AAA96737.
XX
PT Polypeptide expressed in mammalian fsn -/- lymph node stromal cells,
PT useful for modulating growth of blood cells, for treating inflammatory
PT and tumour necrosis factor-mediated disorders, cancer and viral
PT disorders -
XX
PS Claim 1; Page 69-71; 75pp; English.
XX
CC The present sequence represents a polypeptide sequence which is
CC isolated from lymph node stromal cells of fsn -/- mice. The
CC polynucleotides and their polypeptides are useful for treating an
CC inflammatory disorder, disorder of immune system and cancer selected
CC from epithelial, lymphoid, myeloid, stromal and neuronal cancers, a
CC viral disorder, in particular HIV infection and for modulating the
CC growth of blood vessels. The polypeptides are useful for treating a
CC tumour necrosis factor (TNF) mediated disorder, such as those selected
CC from arthritis, inflammatory bowel disease and cardiac failure and a
CC fibroblast growth factor-mediated disorder. It is also useful in assays
CC to determine biological activity, to raise antibodies, to isolate
CC corresponding ligands or receptors, to quantify levels of protein or
CC cognate corresponding ligand or receptors, as antiinflammatory agents,
CC and in compositions for the treatment of skin, connective tissue and
CC immune system diseases. The polynucleotide is useful as marker for
CC tissue, as a chromosome marker or tags in the identification of a
CC genetic disorder.
XX
SQ Sequence 757 AA;

Query Match 87.2%; Score 3645.5; DB 21; Length 757;
Best Local Similarity 86.4%; Pred. No. 0;
Matches 654; Conservative 44; Mismatches 58; Indels 1; Gaps 1;

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Qy       1 MAWSPPATLFLF-LLLLGQPPPSRPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWGTVCD 59
           | |  | |  || |||| | | ||||| || |||||||  :|:||||||||||||||||
Db       1 MMWPQPPTFSLFLLLLLSQAPSSRPQSSGTKKLRLVGPADRPKEGRLEVLHQGQWGTVCD 60

Qy      60 DNFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSNGWGV 119
           |:||:|||||||||||||:|||||||||||||||||||||||:||| :||||||||||:
Db      61 DDFALQEATVACRQLGFESALTWAHSAKYGQGEGPIWLDNVRCLGTEKTLDQCGSNGWGI 120

Qy     120 SDCSHSEDVGVICHPRRHRGYLSETVSNALGPQGRRLEEVRLKPILASAKQHSPVTEGAV 179
           ||| |||||||:|||||  || || |||||||||||||||||||||||:|||||||||
Db     121 SDCRHSEDVGVVCHPRRQHGYHSEKVSNALGPQGRRLEEVRLKPILASAKRHSPVTEGAV 180

Qy     180 EVKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRKVWDLKMRDPKSRLKSLT 239
           ||:|:|||||||||||||||||||||||:  |:||||||||:|||:|||||| |||
Db     181 EVRYDGHWRQVCDQGWTMNNSRVVCGMLGFPSQTSVNSHYYRKVWNLKMKDPKSRLNSLT 240

Qy     240 NKNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHAVVSCVAGPHFRPPKTKP 299
           |||||||:| | |||||:| ||||||| |||| ||||||||||||||||||  | ||
Db     241 KKNSFWIHRVDCFGTEPHLAKCQVQVAPGRGKLRAACPGGMHAVVSCVAGPHFRRQKPKP 300

Qy     300 QRKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVVCRQLGFGSARE 359
           || | ||| :||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TRKESHAEELKVRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVVCRQLGFGSARE 360

Qy     360 ALFGARLGQGLGPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENAAAVRCNVPNMGFQN 419
           |||||:|||||||||||||||||| || |||||||||| | ||||||:|:|||||
Db     361 ALFGAQLGQGLGPIHLSEVRCRGYERTLGDCLALEGSQNGCQHANDAAVRCNIPDMGFQN 420

Qy     420 QVRLAGGRIPEEGLLEVQVEVNGVPRWGSVCSENWGLTEAMVACRQLGLGFAIHAYKETW 479
           :|||||| |||::|||||||||||:|||::|||||||| |||||||| | |:||
Db     421 KVRLAGGRNSEEGVVEVQVEVNGVPRWGTVCSDHWGLTEAMVTCRQLGLGFANFALKDTW 480

Qy     480 FWSGTPRAQEVVMSGVRCSGTELALQQCQRHGPVHCSHGGGRFLAGVSCMDSAPDLVMNA 539
           :| ||| |:|||||||||||:|||||||||||||| ||| |||:||:|||||||||
Db     481 YWQGTPEAKEVVMSGVRCSGTEMALQQCQRHGPVHCSHGPGRFSAGVACMNSAPDLVMNA 540

Qy     540 QLVQETAYLEDRPLSQLYCAHEENCLSKSADHMDWPYGYRRLLRFSTQIYNLGRTDFRPK 599
           |||||||||||||| ||||||||||||||||||||||||:||||||| |||||
Db     541 QLVQETAYLEDRPLSMLYCAHEENCLSKSADHMDWPYGYRRLLRFSSQIYNLGRADFRPK 600

Qy     600 TGRDSWVWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTNCPTGLQRRYACA 659
           || ||:|||||||||||||||||||||||||||||||||||||||:|:|||||||
Db     601 AGRHSWIWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTNCPSGVQRRYACA 660

Qy     660 NFGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAESDFSNNMLQCRC 719
           ||||||| ||||||||||||||||||||||:|||||:|||  :||||||||||::|||
```

```
Db    661 NFGEQGVAVGCWDTYRHDIDCQWVDITDVGPGDYIFQVVVNPTNDVAESDFSNNMIRCRC 720

Qy    720 KYDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI 756
          |||| |||||||||||:|| ||||||||||||||||||
Db    721 KYDGQRVWLHNCHTGDSYRANAELSLEQEQRLRNNLI 757


RESULT 6
ABB07650
ID   ABB07650 standard; Protein; 757 AA.
XX
AC   ABB07650;
XX
DT   20-MAY-2002  (first entry)
XX
DE   Human lysyl-oxidase gene 27 product.
XX
KW   Lysyl-oxidase; angiogenesis; cancer; LOR-1; antiarthritic; antidiabetic;
KW   ophthalmological; antipsoriatic; antiinflammatory; vasotropic; human;
KW   immunomodulator; dermatological; vulnerary; enzyme.
XX
OS   Homo sapiens.
XX
PN   WO200211667-A2.
XX
PD   14-FEB-2002.
XX
PF   07-AUG-2001; 2001WO-IL00728.
XX
PR   08-AUG-2000; 2000US-223739P.
XX
PA   (TECR ) TECHNION RES & DEV FOUND LTD.
XX
PI   Neufeld G,  Akiri G,  Vadasz Z,  Gengrovitch S;
XX
DR   WPI; 2002-227109/28.
XX
PT   Composition for modulating angiogenesis in mammalian tissue for
PT   treating e.g. arthritis, psoriasis, comprises molecule capable of
PT   modifying level and/or activity of at least one type of lysyl-oxidase
PT   of the tissue  -
XX
PS   Claim 7; Page 54-57; 67pp; English.
XX
CC   The invention provides a pharmaceutical composition useful for modulating
CC   angiogenesis in mammalian tissue. The composition comprises a molecule
CC   capable of modifying a level and/or activity of at least one type of
CC   lysyl-oxidase of the mammalian tissue as an active ingredient and a
CC   carrier. Methods for identifying molecules capable of modulating
CC   angiogenesis; for modulating angiogenesis in a mammalian tissue; and for
CC   determining the malignancy of cancerous tissue are also provided, where
CC   the modulation in activity is useful for treating arthritis, diabetic
CC   retinopathy, psoriasis, vasculitis; and for disease characterized by
CC   fragile blood vessels, including Marfans syndrome, Kawasaki, Ehlers-
CC   Danlos, cutis-laxa, and takysu; diseases characterized by changes in the
CC   wall of blood vessels e.g. restenosis which is a common complication
CC   following balloon therapy, fibromuscular dysplasia and aortic stenosis.
CC   The present sequence represents a lysyl-oxidase gene 27 product.
XX
SQ   Sequence   757 AA;

  Query Match             87.1%;  Score 3641.5;  DB 23;  Length 757;
  Best Local Similarity   86.4%;  Pred. No. 0;
  Matches  654;  Conservative   43;  Mismatches   59;  Indels    1;  Gaps    1;

Qy      1 MAWSPPATLFLF-LLLLGQPPPSRPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWGTVCD 59
          | |  | |  || |||| | | ||||| || |||||||  :||||||||||||||||||||
Db      1 MMWPQPPTFSLFLLLLLSQAPSSRPQSSGTKKLRLVGPADRPEEGRLEVLHQGQWGTVCD 60

Qy     60 DNFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSNGWGV 119
          ||:||:|||||||||||||:|||||||||||||||||||||:||| :||||||||||:
Db     61 DDFALQEATVACRQLGFESALTWAHSAKYGQGEGPIWLDNVRCLGTEKTLDQCGSNGWGI 120

Qy    120 SDCSHSEDVGVICHPRRHRGYLSETVSNALGPQGRRLEEVRLKPILASAKQHSPVTEGAV 179
          ||| |||||||:|||||  || || ||||||||||||||||||||:|||||||||
Db    121 SDCRHSEDVGVVCHPRRQHGYHSEKVSNALGPQGRRLEEVRLKPILASAKRHSPVTEGAV 180

Qy    180 EVKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRKVWDLKMRDPKSRLKSLT 239
          ||:|:|||||||||||||||||||||||||||:  |:||||||||:|||:|||||| |||
Db    181 EVRYDGHWRQVCDQGWTMNNSRVVCGMLGFPSQTSVNSHYYRKVWNLKMKDPKSRLNSLT 240

Qy    240 NKNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHAVVSCVAGPHFRPPKTKP 299
          |||||||:| | |||||:| ||||||| ||||||||||||||||||||||||  | ||
Db    241 KKNSFWIHRVDCFGTEPHLAKCQVQVAPGRGKLRPACPGCMHAVVSCVAGPHFRRQKPKP 300

Qy    300 QRKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGTVCDHFWNLISASVVCRQLGFGSARE 359
          || | ||| :||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TRKESHAEELKVRLRSGAQVGEGRVEVLMNRQWGTVCDHFWNLISASVVCRQLGFGSARE 360

Qy    360 ALFGARLGQGLGPIHLSEVRCRGYERTLSDCPALEGSQNCQHENAAAVRCNVPNMGFQN 419
          |||||:|||||||||||||||||||||| || |||||||:||| | |||||||:|:|||||
Db    361 ALFGAQLGQGLGPIHLSEVRCRGYERTLGDCLALEGSQNCQHANDAAVRCNIPDMGFQN 420

Qy    420 QVRLAGGRIPEEGLLEVQVEVNGVPRWGSVCSENWGLTEAMVACRQLGLGFAIHAYKETW 479
          :|||||||  |||::|||||||| ||||:|||::|||||| || |||||||:  | |:||
Db    421 KVRLAGGRNSEEGVVEVQVEVNGGPRWGTVCSDHWGLTEAMVTCRQLGLGFANFAILKDTW 480

Qy    480 FWSGTPRAQEVVMSGVRCSGTELALQQCQRHGPVHCSHGQGRFLAGVSCMDSAPDLVMNA 539
          :| ||| |:|||||||||||:|||||||||||||||| ||| |||:||:|||||||||
Db    481 YWQGTPEAKEVVMSGVRCSGTEMALQQCQRHGPVHCSHGPGRFSAGVACMNSAPDLVMNA 540

Qy    540 QLVQETAYLEDRPLSQLYCAHEENCLSKSADHMDWPYGYRRLLRFSTQIYNLGRTDFRPK 599
          |||||||||||||| ||||||||||||||||||||||||||:|||||| ||||
Db    541 QLVQETAYLEDRPLSMLYCAHEENCLSKSADHMDWPYGYRRLLRFSSQIYNLGRADFRPK 600

Qy    600 TGRDSWVWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTNCPTGLQRRYACA 659
          || ||:|||||| ||||||||||||||||||||||||||||||||||:|:|||||||
Db    601 AGRHSWIWHQCHRHNHSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTNCPSGVQRRYACA 660

Qy    660 NFGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAESDFSNNMLQCRC 719
          ||||||| ||||||||||||||||||||||:|||||:|||  :|||||||||::|||
Db    661 NFGEQGVAVGCWDTYRHDIDCQWVDITDVGPGDYIFQVVVNPTNDVAESDFSNNMIRCRC 720

Qy    720 KYDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI 756
          |||| |||||||||||:|| ||||||||||||||||||
Db    721 KYDGQRVWLHNCHTGDSYRANAELSLEQEQRLRNNLI 757


RESULT 7
AAB49534
ID   AAB49534 standard; Protein; 573 AA.
XX
AC   AAB49534;
XX
DT   09-MAR-2001  (first entry)
XX
DE   Clone HOHEC84 #1.
XX
KW   Gene therapy; human; bone morphogenic protein; neural disorder; immune;
KW   muscular; reproductive; gastrointestinal; pulmonary; cardiovascular;
KW   renal; proliferative; wound healing; infectious disease; thrombosis;
KW   arthritis; infertility.
XX
OS   Homo sapiens.
XX
PN   WO200061774-A2.
XX
PD   19-OCT-2000.
XX
PF   06-APR-2000; 2000WO-US09028.
XX
PR   09-APR-1999;   99US-0128701.
PR   23-APR-1999;   99US-0130693.
PR   29-APR-1999;   99US-0131672.
PR   11-JUN-1999;   99US-0138632.
PR   03-AUG-1999;   99US-0147020.
```

```
PR   09-SEP-1999;   99US-0152933.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Ni J,  Komatsoulis G,  Rosen CA,  Shi Y;
XX
DR   WPI; 2000-656328/63.
DR   N-PSDB; AAC90026.
XX
PT   Bone morphogenic proteins and nucleic acid sequences encoding them,
PT   useful for detecting, preventing and treating cancers and neurological,
PT   immune system and cardiovascular disorders -
XX
PS   Claim 11; Pages 277-279; 291pp; English.
XX
CC   The present invention relates to isolated coding sequences and proteins
CC   for human bone morphogenic proteins (BMPs) (see AAC90025-C90030 and
CC   AAB49533-B49538). The present sequence is one such protein sequence.
CC   This sequence may be used to treat disorders such as neural, immune,
CC   muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC   renal, and proliferative disorders (numerous examples of each type of
CC   disorder are given in the specification), wounds, infectious diseases,
CC   thrombosis, arthritis, and infertility.
XX
SQ   Sequence   573 AA;

  Query Match             72.9%;  Score 3047.5;  DB 21;  Length 573;
  Best Local Similarity   98.6%;  Pred. No. 3.6e-271;
  Matches  563;  Conservative    0;  Mismatches    3;  Indels    5;  Gaps    2;

Qy       1 MAWSPPATLFLFLLLLGQPPPSRPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWGTVCDD 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAWSPPATLFLFLLLLGQPPPSRPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWGTVCDD 60

Qy      61 NFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSNGWGVS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 NFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSNGWGVS 120

Qy     121 DCSHSEDVGVICHPRRHRGYLSETVSNALGPQ--GRRLEEVRLKPILASAKQHSPVTEGA 178
           ||||||||||||||||||||||||||||||||  | |    ||||||||||||||||||||
Db     121 DCSHSEDVGVICHPRRHRGYLSETVSNALGPQAGGWR---GRLKPILASAKQHSPVTEGA 177

Qy     179 VEVKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRKVWDLKMRDPKSRLKSL 238
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     178 VEVKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRKVWDLKMRDPKSRLKSL 237

Qy     239 TNKNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHAVVSCVAGPHFRPPKTK 298
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     238 TNKNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHAVVSCVAGPHFRPPKTK 297

Qy     299 PQRKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVVCRQLGFGSAR 358
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     298 PQRKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVVCRQLGFGSAR 357

Qy     359 EALFGARLGQGLGPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENAAAVRCNVPNMGFQ 418
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     358 EALFGARLGQGLGPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENDAAVRCNVPNMGFQ 417

Qy     419 NQVRLAGGRIPEEGLLEVQVEVNGVPRWGSVCSENWGLTEAMVACRQLGLGFAIHAYKET 478
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     418 NQVRLAGGRIPEEGLLEVQVEVNGVPRWGSVCSENWGLTEAMVACRQLGLGFAIHAYKET 477

Qy     479 WFWSGTPRAQEVVMSGVRCSGTELALQQCQRHGPVHCSHGGGRFLAGVSCMDSAPDLVMN 538
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     478 WFWSGTPRAQEVVMSGVRCSGTELALQQCQRHGPVHCSHGGGRFLAGVSCMDSAPDLVMN 537

Qy     539 AQLVQETAYLEDRPLSQLYCAHEENCLSKSA 569
           |||||||||||||||||||||||||||||||
Db     538 AQLVQETAYLEDRPLSQLYCAHEENCLSKSA 568


RESULT 8
AAE11940
ID   AAE11940 standard; Protein; 769 AA.
XX
AC   AAE11940;
XX
DT   18-DEC-2001  (first entry)
XX
DE   Human lipid metabolism related protein #3.
XX
KW   Human; apolipoprotein; lipase; lipoprotein receptor; ALLr; angina;
KW   cardiovascular disease; lipid metabolism; myocardial infarction;
KW   cerebral ischaemia; arterial thrombosis; thrombolytic; antilipaemic;
KW   coronary artery thrombosis; cerebral artery thrombosis; stroke;
KW   intracardiac thrombosis; gene therapy; cardiovascular; vasodilator;
KW   neuroprotectant; cerebroprotective.
XX
OS   Homo sapiens.
XX
PN   WO200179446-A2.
XX
PD   25-OCT-2001.
XX
PF   16-APR-2001; 2001WO-US12529.
XX
PR   14-APR-2000; 2000US-197137P.
PR   20-JUN-2000; 2000US-0598042.
PR   03-AUG-2000; 2000US-0631451.
PR   22-SEP-2000; 2000US-0667298.
PR   17-NOV-2000; 2000US-0714936.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Ballinger DG,  Loeb D,  Montgomery JR,  Tang TY,  Zhou P,  Goodrich R;
PI   Liu C,  Asundi V,  Zhao QA,  Wehrman T,  Drmanac RT,  Ren F,  Qian XB;
PI   Wang D;
XX
DR   WPI; 2001-611724/70.
DR   N-PSDB; AAD19235.
XX
PT   Nucleic acids encoding human apolipoproteins, lipases, and lipoprotein
PT   receptor polypeptides, useful for preventing diagnosing and treating
PT   lipid metabolism disorders, thrombosis and cardiovascular diseases -
XX
PS   Claim 10; Page 257-259; 266pp; English.
XX
CC   The invention relates to polynucleotides encoding proteins CG122, CG179,
CC   CG95, CG121, CG162, CG27, CG153 and CG168 which are related to proteins
CC   involved in lipid metabolism and cardiovascular disease such as human
CC   apolipoproteins, lipases and lipoprotein receptor proteins. These DNA
CC   and protein sequences are useful for treating or preventing disorders
CC   associated with apolipoproteins, lipases and lipoprotein receptor (ALLr)
CC   expression and for treating lipid metabolism, cardiovascular diseases
CC   and thrombosis. Antibodies against these proteins are useful for
CC   determining the presence of or predisposition to a disease associated
CC   with altered levels of these sequences. ALLr polypeptides are also
CC   useful for identifying agents (agonists and antagonists) that bind to
CC   them and cells expressing ALLr proteins are useful for identifying a
CC   therapeutic agent for use in treatment of a pathology related to
CC   aberrant expression or physiological interactions of this polypeptide.
CC   Vectors comprising these DNA and protein sequences are also useful for
CC   producing ALLr proteins. The nucleic acids and polypeptides of the
CC   invention are also useful for the treatment of occlusive cardiovascular
CC   diseases, myocardial infarction, cerebral ischaemia, angina, arterial
CC   thrombosis, coronary artery thrombosis and cerebral artery thrombosis
CC   or intracardiac thrombosis and stroke. The nucleotides of the invention
CC   are used in gene therapy. The present sequence is human protein
CC   related to proteins involved in lipid metabolism.
XX
SQ   Sequence   769 AA;

  Query Match             54.5%;  Score 2278.5;  DB 22;  Length 769;
  Best Local Similarity   55.1%;  Pred. No. 3.2e-200;
  Matches  422;  Conservative  106;  Mismatches  205;  Indels   33;  Gaps   11;
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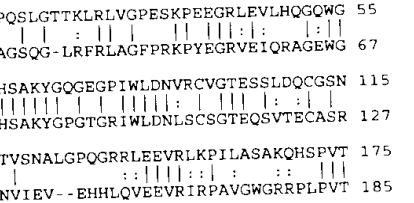
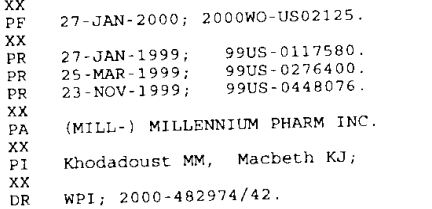
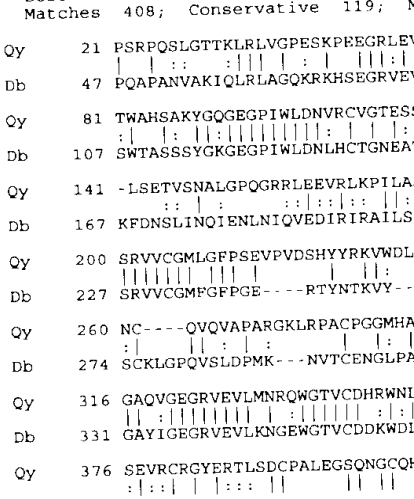


RESULT 9
AAB00077
ID AAB00077 standard; Protein; 774 AA.
XX
AC AAB00077;
XX
DT 08-NOV-2000 (first entry)
XX
DE Human lysyl oxidase related protein (Lor).
XX
KW Lysyl oxidase; lysyl oxidase like protein; lox; lol; collagen;
KW lysyl oxidase related protein; lor; lor-2; elastin; bone;
KW connective tissue; congestive heart failure; ischaemia;
KW cardiac hypertrophy; ischaemic-reperfusion injury.
XX
OS Homo sapiens.
XX
PN WO200044910-A1.
XX
PD 03-AUG-2000.



XX
PF 27-JAN-2000; 2000WO-US02125.
XX
PR 27-JAN-1999; 99US-0117580.
PR 25-MAR-1999; 99US-0276400.
PR 23-NOV-1999; 99US-0448076.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Khodadoust MM, Macbeth KJ;
XX
DR WPI; 2000-482974/42.
XX
PT New nucleic acid molecule encoding a lysyl oxidase related-2 (Lor-2)
PT protein useful in the treatment of cardiovascular disorders e.g.
PT cardiac hypertrophy
XX
PS Disclosure; Fig 5a-d; 148pp; English.
XX
CC Lysyl oxidase (Lox) is an extracellular copper enzyme that
CC initiates the crosslinking of collagens and elastin by catalysing
CC oxidative deamination of the epsilon-amino group in certain lysine
CC and hydroxylysine residues of collagens and lysine residues of
CC elastin. Lox has been shown to be important in a variety of cellular
CC and physiologic processes including biogenesis of connective tissue
CC matrices and bone resorption. A lysyl oxidase like protein (Lol) was
CC also identified from a human skin fibroblast cDNA library and contains
CC extensive homology to several coding domains within the human Lox
CC mRNA. Lol is believed to be involved in collagen maturation. A Lysyl
CC oxidase related protein (Lor) has now been identified which inhibits
CC many of the structural features of lysyl oxidase and is overexpressed
CC in senescent fibroblasts. It is believed to play a role in age
CC associated changes in extracellular proteins. Lor contains four
CC domains referred to as scavenger receptor cysteine-rich domains
CC (SRCR domains) which are believed to be involved in cell binding to
CC other cell surface proteins or extracellular molecules. The nucleic
CC acids encoding Lor, Lor proteins and antibodies directed against them
CC are particularly useful in the treatment of cardiovascular disorders
CC e.g. congestive heart failure, ischaemia, cardiac hypertrophy and
CC ischaemic-reperfusion injury.
XX
SQ Sequence 774 AA;

Query Match 54.3%; Score 2268.5; DB 21; Length 774;
Best Local Similarity 55.1%; Pred. No. 2.7e-199;
Matches 408; Conservative 119; Mismatches 190; Indels 23; Gaps 7;



```
Db     391 NEIQCTGNEKSIIDCKFNAESQ-GCNHEEDAGVRCNTPAMGLQKKLRLNGGRNPYEGRVE 449

Qy     436 VQVEVNGVPRWGSVCSENWGLTEAMVACRQLGLGFAIHAYKETWFWSGTPRAQEVVMSGV 495

Db     450 VLVERNGSLVWGMVCGQNWGIVEAMVVCRQLGLGFASNAFQETWYWHGDVNSNKVVMSGV 509

Qy     496 RCSGTELALQQCQRHG-PVHCSHGGGRFLAGVSCMDSAPDLVMNAQLVQETAYLEDRPLS 554

Db     510 KCSGTELSLAHCRHDGEDVACPQGGVQYGAGVACSETAPDLVLNAEMVQQTTYLEDRPMF 569

Qy     555 QLYCAHEENCLSKSADHMDWPYGYRRLLRFSTQIYNLGRTDFRPKTGRDSWVWHQCHRHY 614

Db     570 MLQCAMEENCLSASAAQTDPTTGYRRLLRFSSQIHNNGQSDFRPKNGRHAWIWHDCHRHY 629

Qy     615 HSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTNCPTGLQRRYACANFGEQGVTVGCWDTY 674

Db     630 HSMEVFTHYDLLNLNGTKVAEGHKASFCLEDTECEGDIQKNYECANFGDQGITMGCWDMY 689

Qy     675 RHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAESDFSNNMLQCRCKYDGHRVWLHNCHTG 734

Db     690 RHDIDCQWVDITDVPPGDYLFQVVINPNFEVAESDYSNNIMKCRSRYDGHRIWMYNCHIG 749

Qy     735 NSYPANAELSLEQEQRLRNN 754

Db     750 GSFSEETEKKFEHFSGLLNN 769
```

RESULT 10
ABB07649
ID ABB07649 standard; Protein; 774 AA.
XX
AC ABB07649;
XX
DT 20-MAY-2002 (first entry)
XX
DE Human LOR-1 protein.
XX
KW Lysyl-oxidase; angiogenesis; cancer; LOR-1; antiarthritic; antidiabetic;
KW ophthalmological; antipsoriatic; antiinflammatory; vasotropic; human;
KW immunomodulator; dermatological; vulnerary; enzyme.
XX
OS Homo sapiens.
XX
PN WO200211667-A2.
XX
PD 14-FEB-2002.
XX
PF 07-AUG-2001; 2001WO-IL00728.
XX
PR 08-AUG-2000; 2000US-223739P.
XX
PA (TECR) TECHNION RES & DEV FOUND LTD.
XX
PI Neufeld G, Akiri G, Vadasz Z, Gengrovitch S;
XX
DR WPI; 2002-227109/28.
DR N-PSDB; ABA95142.
XX
PT Composition for modulating angiogenesis in mammalian tissue for
PT treating e.g. arthritis, psoriasis, comprises molecule capable of
PT modifying level and/or activity of at least one type of lysyl-oxidase
PT of the tissue -
XX
PS Claim 7; Page 51-54; 67pp; English.
XX
CC The invention provides a pharmaceutical composition useful for modulating
CC angiogenesis in mammalian tissue. The composition comprises a molecule
CC capable of modifying a level and/or activity of at least one type of
CC lysyl-oxidase of the mammalian tissue as an active ingredient and a
CC carrier. Methods for identifying molecules capable of modulating
CC angiogenesis; for modulating angiogenesis in a mammalian tissue; and for
CC determining the malignancy of cancerous tissue are also provided, where
CC the modulation in activity is useful for treating arthritis, diabetic
CC retinopathy, psoriasis, vasculitis; and for disease characterized by
CC fragile blood vessels, including Marfans syndrome, Kawasaki, Ehlers-
CC Danlos, cutis-laxa, and takysu; diseases characterized by changes in the
CC wall of blood vessels e.g. restenosis which is a common complication
CC following balloon therapy, fibromuscular dysplasia and aortic stenosis.
CC The present sequence represents a LOR-1 protein, belonging to the lysyl
CC -oxidase family of enzymes.
XX
SQ Sequence 774 AA;

Query Match 54.3%; Score 2268.5; DB 23; Length 774;
Best Local Similarity 55.1%; Pred. No. 2.7e-199;
Matches 408; Conservative 119; Mismatches 190; Indels 23; Gaps 7;

```
Qy      21 PSRPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWGTVCDDNFAIQEATVACRQLGFEAAL 80

Db      47 PQAPANVAKIQLRLAGQKRKHSEGRVEVYYDGQWGTVCDDDFSIHAAHVVCRELGYVEAK 106

Qy      81 TWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSNGWGVSDCSHSEDVGVICHPRRHRGY 140

Db     107 SWTASSSYGKGEGPIWLDNLHCTGNEATLAACTSNGWGVTDCKHTEDVGVVCSDKRIPGF 166

Qy     141 -LSETVSNALGPQGRRLEEVRLKPILASAKQHSPVTEGAVEVKYEGHWRQVCDQGWTMNN 199

Db     167 KFDNSLINQIENLNIQVEDIRIRAILSTYRKRTPVMEGYVEVKEGKTWKQICDKHWTAKN 226

Qy     200 SRVVCGMLGFPSEVPVDSHYYRKVWDLKMRDPKSRLKSLTNKNSFWIHQVTCLGTEPHMA 259

Db     227 SRVVCGMFGFPGE----RTYNTKVY---------KMFASRRKQRYWPFSMDCTGTEAHIS 273

Qy     260 NC----QVQVAPARGKLRPACPGGMHAVVSCVAGPHFRPPKTKPQRKGSWAEEPRVRLRS 315

Db     274 SCKLGPQVSLDPMK---NVTCENGLPAVVSCVPGQVFSPDGPSRFRKAYKPEQPLVRLRG 330

Qy     316 GAQVGEGRVEVLMNRQWGTVCDHRWNLISASVVCRQLGFGSAREALFGARLGQGLGPIHL 375

Db     331 GAYIGEGRVEVLKNGEWGTVCDDKWDLVSASVVCRELGFGSAKEAVTGSRLGQGIGPIHL 390

Qy     376 SEVRCRGYERTLSDCPALEGSQNGCQHENAAAVRCNVPNMGFQNQVRLAGGRIPEEGLLE 435

Db     391 NEIQCTGNEKSIIDCKFNAESQ-GCNHEEDAGVRCNTPAMGLQKKLRLNGGRNPYEGRVE 449

Qy     436 VQVEVNGVPRWGSVCSENWGLTEAMVACRQLGLGFAIHAYKETWFWSGTPRAQEVVMSGV 495

Db     450 VLVERNGSLVWGMVCGQNWGIVEAMVVCRQLGLGFASNAFQETWYWHGDVNSNKVVMSGV 509

Qy     496 RCSGTELALQQCQRHG-PVHCSHGGGRFLAGVSCMDSAPDLVMNAQLVQETAYLEDRPLS 554

Db     510 KCSGTELSLAHCRHDGEDVACPQGGVQYGAGVACSETAPDLVLNAEMVQQTTYLEDRPMF 569

Qy     555 QLYCAHEENCLSKSADHMDWPYGYRRLLRFSTQIYNLGRTDFRPKTGRDSWVWHQCHRHY 614

Db     570 MLQCAMEENCLSASAAQTDPTTGYRRLLRFSSQIHNNGQSDFRPKNGRHAWIWHDCHRHY 629

Qy     615 HSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTNCPTGLQRRYACANFGEQGVTVGCWDTY 674

Db     630 HSMEVFTHYDLLNLNGTKVAEGHKASFCLEDTECEGDIQKNYECANFGDQGITMGCWDMY 689

Qy     675 RHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAESDFSNNMLQCRCKYDGHRVWLHNCHTG 734

Db     690 RHDIDCQWVDITDVPPGDYLFQVVINPNFEVAESDYSNNIMKCRSRYDGHRIWMYNCHIG 749

Qy     735 NSYPANAELSLEQEQRLRNN 754

Db     750 GSFSEETEKKFEHFSGLLNN 769
```

RESULT 11
ABB07653
ID ABB07653 standard; Protein; 752 AA.
XX
AC ABB07653;
XX

```
DT   20-MAY-2002  (first entry)
XX
DE   Human lysyl-oxidase gene 33 product.
XX
KW   Lysyl-oxidase; angiogenesis; cancer; LOR-1; antiarthritic; antidiabetic;
KW   ophthalmological; antipsoriatic; antiinflammatory; vasotropic; human;
KW   immunomodulator; dermatological; vulnerary; enzyme.
XX
OS   Homo sapiens.
XX
PN   WO200211667-A2.
XX
PD   14-FEB-2002.
XX
PF   07-AUG-2001; 2001WO-IL00728.
XX
PR   08-AUG-2000; 2000US-223739P.
XX
PA   (TECR ) TECHNION RES & DEV FOUND LTD.
XX
PI   Neufeld G,  Akiri G,  Vadasz Z,  Gengrovitch S;
XX
DR   WPI; 2002-227109/28.
XX
PT   Composition for modulating angiogenesis in mammalian tissue for
PT   treating e.g. arthritis, psoriasis, comprises molecule capable of
PT   modifying level and/or activity of at least one type of lysyl-oxidase
PT   of the tissue  -
XX
PS   Claim 7; Page 64-67; 67pp; English.
XX
CC   The invention provides a pharmaceutical composition useful for modulating
CC   angiogenesis in mammalian tissue. The composition comprises a molecule
CC   capable of modifying a level and/or activity of at least one type of
CC   lysyl-oxidase of the mammalian tissue as an active ingredient and a
CC   carrier. Methods for identifying molecules capable of modulating
CC   angiogenesis; for modulating angiogenesis in a mammalian tissue; and for
CC   determining the malignancy of cancerous tissue are also provided, where
CC   the modulation in activity is useful for treating arthritis, diabetic
CC   retinopathy, psoriasis, vasculitis; and for disease characterized by
CC   fragile blood vessels, including Marfans syndrome, Kawasaki, Ehlers-
CC   Danlos, cutis-laxa, and takysu; diseases characterized by changes in the
CC   wall of blood vessels e.g. restenosis which is a common complication
CC   following balloon therapy, fibromuscular dysplasia and aortic stenosis.
CC   The present sequence represents a lysyl-oxidase gene 33 product.
XX
SQ   Sequence   752 AA;

  Query Match             54.1%;  Score 2263;  DB 23;  Length 752;
  Best Local Similarity   54.5%;  Pred. No. 8.3e-199;
  Matches  419;  Conservative  105;  Mismatches  205;  Indels   40;  Gaps   10;

Qy          3 WSPPATLFLFLL--LLGQPPPS-----RPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWG 55
                |||  |    |     || | ||        :  | |   : ||  |     || |||:|:    |:||
Db          9 WSPWGLLLCLLCSSCLGSPSPSTGPEKKAGSQG-LRFRLAGFPRKPYEGRVEIQRAGEWG 67

Qy         56 TVCDDNFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSN 115
              |:|||:|  :|   |  ||:|||   |   |||||| |  ||||: | ||  |:  :|
Db         68 TICDDDFTLQAAHILCRELGFTEATGWTHSAKYGPGTGRIWLDNLSCSGTEQSVTECASR 127

Qy        116 GWGVSDCSHSEDVGVICHPRRHRGYLSETVSNALGPQGRRLEEVRLKPILASAKQHSPVT 175
              ||| |||:| || ||||  :|   |:    |               ::||||:: |  :   ::  |||
Db        128 GWGNSDCTHDEDAGVICKDQRLPGFSDSNVIEV--EHHLQVEEVRIRPAVGWGRRPLPVT 185

Qy        176 EGAVEVKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRKVWDLKMRDPKSRL 235
              || |||:    |   ||||:||:   |:|||||||||||  |::  :|                 ||
Db        186 EGLVEVRLPDGWSQVCDKGWSAHNSHVVCGMLGFPSEKRVNAAFY-------------RL 232

Qy        236 KSLTNKNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHAVVSCVAGPHF--- 292
                :   ::||  :|  |:|||  |:: |  : :      |      |   ||||   ||||||  ||  :
Db        233 LAQRQQHSFGLHGVACVGTEAHLSLCSLEFYRANDTAR--CPGGGPAVVSCVPGPVYAAS 290

Qy        293 ----RPPKTKPQRKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVV 348
                    :  ::|||          | ||||: ||   ||||||||    ||||| :|:| :||||
Db        291 SGQKKQQQSKPQ------GEARVRLKGGAHPGEGRVEVLKASTWGTVCDRKWDLHAASVV 344

Qy        349 CRQLGFGSAREALFGARLGQGLGPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENAAAV 408
              ||:||||||||||| |||:|||:| ||||||| |  :|   ||       :      |      |
Db        345 CRELGFGSAREALSGARMGQGMGAIHLSEVRCSGQELSLWKCPHKNITAEDCSHSQDAGV 404

Qy        409 RCNVPNMGFQNQVRLAGGRIPEEGLLEVQVEVNGVPRWGSVCSENWGLTEAMVACRQLGL 468
              |||:|   |  :  ::||:|||      ||  :|||:      |   |||  :|  ::||   ||||||||||
Db        405 RCNLPYTGAETRIRLSGGRSQHEGRVEVQIGGPGPLRWGIICGDDWGTLEAMVACRQLGL 464

Qy        469 GFAIHAYKETWFWSGTPRAQEVVMSGVRCSGTELALQQCQRHGP-VHCSHGGGRFLAGVS 527
              |:|   :|||:|    :    ||||||||:||||:|  ||      ||    :     ||  |||
Db        465 GYANHGLQETWYWD-SGNITEVVMSGVRCTGTELSLDQCAHHGTHITCKRTGTRFTAGVI 523

Qy        528 CMDSAPDLVMNAQLVQETAYLEDRPLSQLYCAHEENCLSKSADHMDWPYGYRRLLRFSTQ 587
              |  ::|  ||::::    |||||||:|||||    ||||   |||||:  ||      :|||:|||||||:|
Db        524 CSETASDLLLHSALVQETAYIEDRPLHMLYCAAEENCLASSARSANWPYGHRRLLRFSSQ 583

Qy        588 IYNLGRTDFRPKTGRDSWVWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTN 647
              |:||||  |||||  ||  ||||||:||  ||||:::||||||:|   ||:||||||||||||||
Db        584 IHNLGRADFRPKAGRHSWVWHECHGHYHSMDIFTHYDILTPNGTKVAEGHKASFCLEDTE 643

Qy        648 CPTGLQRRYACANFGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAE 707
              |    : :||  ||||||||:||||||  ||||||||||  |||||  ||||:::||::||||
Db        644 CQEDVSKRYECANFGEQGITVGCWDLYRHDIDCQWIDITDVKPGNYILQVVINPNFEVAE 703

Qy        708 SDFSNNMLQCRCKYDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI 756
              |||:|| ::|| |||||||:|:||||  |:::        |         |:               :|  |
Db        704 SDFTNNAMKCNCKYDGHRIWVHNCHIGDAFSEEANRRFERYPGQTSNQI 752


RESULT 12
AAB00073
ID   AAB00073 standard; Protein; 753 AA.
XX
AC   AAB00073;
XX
DT   08-NOV-2000  (first entry)
XX
DE   Human lysyl oxidase related protein (Lor)-2
XX
KW   Lysyl oxidase; lysyl oxidase like protein; lox; lol; collagen;
KW   lysyl oxidase related protein; lor; lor-2; elastin; bone;
KW   connective tissue; congestive heart failure  ischaemia;
KW   cardiac hypertrophy; ischaemic-reperfusion  injury.
XX
OS   Homo sapiens.
XX
PN   WO200044910-A1.
XX
PD   03-AUG-2000.
XX
PF   27-JAN-2000; 2000WO-US02125.
XX
PR   27-JAN-1999;    99US-0117580.
PR   25-MAR-1999;    99US-0276400.
PR   23-NOV-1999;    99US-0448076.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Khodadoust MM,  Macbeth KJ;
XX
DR   WPI; 2000-482974/42.
DR   N-PSDB; AAA47798, AAA47799.
XX
PT   New nucleic acid molecule encoding a lysyl oxidase related-2 (Lor 2)
PT   protein useful in the treatment of cardiovascular disorders e.g.
PT   cardiac hypertrophy
XX
PS   Claim 4; Fig 3; 148pp; English.
XX
CC   Lysyl oxidase (Lox) is an extracellular copper enzyme that
```

```
CC   initiates the crosslinking of collagens and elastin by catalysing
CC   oxidative deamination of the epsilon-amino group in certain lysine
CC   and hydroxylysine residues of collagens and lysine residues of
CC   elastin. Lox has been shown to be important in a variety of cellular
CC   and physiologic processes including biogenesis of connective tissue
CC   matrices and bone resorption. A lysyl oxidase like protein (Lol) was
CC   also identified from a human skin fibroblast cDNA library and contains
CC   extensive homology to several coding domains within the human Lox
CC   mRNA. Lol is believed to be involved in collagen maturation. A Lysyl
CC   oxidase related protein (Lor) has now been identified which inhibits
CC   many of the structural features of lysyl oxidase and is overexpressed
CC   in senescent fibroblasts. It is believed to play a role in age
CC   associated changes in extracellular proteins. Lor contains four
CC   domains referred to as scavenger receptor cysteine-rich domains
CC   (SRCR domains) which are believed to be involved in cell binding to
CC   other cell surface proteins or extracellular molecules. The nucleic
CC   acids encoding Lor, Lor proteins and antibodies directed against them
CC   are particularly useful in the treatment of cardiovascular disorders
CC   e.g. congestive heart failure, ischaemia, cardiac hypertrophy and
CC   ischaemic-reperfusion injury.
XX
SQ   Sequence   753 AA;

  Query Match            54.1%;  Score 2263;  DB 21;  Length 753;
  Best Local Similarity  54.5%;  Pred. No. 8.3e-199;
  Matches  419;  Conservative  105;  Mismatches  205;  Indels   40;  Gaps   10;

Qy       3 WSPPATLFLFLL--LLGQPPPS-----RPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWG 55
Db       9 WSPWGLLLCLLCSSCLGSPSPSTGPEKKAGSQG-LRFRLAGFPRKPYEGRVEIQRAGEWG 67

Qy      56 TVCDDNFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSN 115
Db      68 TICDDDFTLQAAHILCRELGFTEATGWTHSAKYGPGTGRIWLDNLSCSGTEQSVTECASR 127

Qy     116 GWGVSDCSHSEDVGVICHPRRHRGYLSETVSNALGPQGRRLEEVRLKPILASAKQHSPVT 175
Db     128 GWGNSDCTHDEDAGVICKDQRLPGFSDSNVIEV--EHHLQVEEVRIRPAVGWGRRPLPVT 185

Qy     176 EGAVEVKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRKVWDLKMRDPKSRL 235
Db     186 EGLVEVRLPDGWSQVCDKGWSAHNSHVVCGMLGFPSEKRVNAAFY-------------RL 232

Qy     236 KSLTNKNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHAVVSCVAGPHF--- 292
Db     233 LAQRQQHSFGLHGVACVGTEAHLSLCSLEFYRANDTAR--CPGGGPAVVSCVPGPVYAAS 290

Qy     293 ----RPPKTKPQRKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVV 348
Db     291 SGQKKQQQSKPQ------GEARVRLKGGAHPGEGRVEVLKASTWGTVCDRKWDLHAASVV 344

Qy     349 CRQLGFGSAREALFGARLGQGLGPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENAAAV 408
Db     345 CRELGFGSAREALSGARMGQGMGAIHLSEVRCSGQELSLWKCPHKNITAEDCSHSQDAGV 404

Qy     409 RCNVPNMGFQNQVRLAGGRIPEEGLLEVQVEVNGVPRWGSVCSENWGLTEAMVACRQLGL 468
Db     405 RCNLPYTGAETRIRLSGGRSQHEGRVEVQIGGPGPLRWGLICGDDWGTLEAMVACRQLGL 464

Qy     469 GFAIHAYKETWFWSGTPRAQEVVMSGVRCSGTELALQQCQRHGP-VHCSHGGGRFLAGVS 527
Db     465 GYANHGLQETWYWD-SGNITEVVMSGVRCTGTELSLDQCAHHGTHITCKRTGTRFTAGVI 523

Qy     528 CMDSAPDLVMNAQLVQETAYLEDRPLSQLYCAHEENCLSKSADHMDWPYGYRRLLRFSTQ 587
Db     524 CSETASDLLLHSALVQETAYIEDRPLHMLYCAAEENCLASSARSANWPYGHRRLLRFSSQ 583

Qy     588 IYNLGRTDFRPKTGRDSWVWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTN 647
Db     584 IHNLGRADFRPKAGRHSWVWHECHGHYHSMDIFTHYDILTPNGTKVAEGHKASFCLEDTE 643

Qy     648 CPTGLQRRYACANFGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAE 707
```

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Db     644 CQEDVSKRYECANFGEQGITVGCWDLYRHDIDCQWIDITDVKPGNYILQVVINPNFEVAE 703

Qy     708 SDFSNNMLQCRCKYDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI 756
Db     704 SDFTNNAMKCNCKYDGHRIWVHNCHIGDAFSEEANRRFERYPGQTSNQI 752


RESULT 13
AAG65903
ID   AAG65903 standard; protein; 753 AA.
XX
AC   AAG65903;
XX
DT   11-FEB-2002  (first entry)
XX
DE   Amino acid sequence of GSK gene Id 14849.
XX
KW   Peptide hormone; antidiabetic; anorectic; antianorectic; antiasthmatic;
KW   antidepressant; nootropic; neuroprotectant; hypotensive; hypertensive;
KW   cytostatic; cerebroprotective; vasotropic; human.
XX
OS   Homo sapiens.
XX
PN   WO200172961-A2.
XX
PD   04-OCT-2001.
XX
PF   22-MAR-2001; 2001WO-US09226.
XX
PR   24-MAR-2000; 2000US-192158P.
PR   28-MAR-2000; 2000US-192668P.
PR   27-APR-2000; 2000US-200166P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Agarwal P,  Murdoch PR,  Rizvi SK,  Smith RF,  Xiang Z,  Kabnick KS;
PI   Lai Y;
XX
DR   WPI; 2001-639223/73.
DR   N-PSDB; AAI67193.
XX
PT   Isolated polypeptides, which may be peptide hormones, which are
PT   identified by high throughput genome-based biology which identifies
PT   genes and gene products as therapeutic targets for treatment of
PT   diseases such as diabetes and cancer  -
XX
PS   Claim 1; Page 79-80; 99pp; English.
XX
CC   The invention provides polypeptides (AAG65886-65918) which may be peptide
CC   hormones (including insulin, growth hormones, chemokines, cytokines,
CC   neuropeptides, integrins, kallikreins, lamins, melanins, natruiretic
CC   hormones, neuropepsin, pituitary hormones, pleiotrophins, prostaglandins,
CC   secretogranins, selectins, thromboglobulins, thymosins) identified by
CC   high throughput genome-based biology and polynucleotides (AAI67176-67208)
CC   encoding them. The polypeptides can be expressed by standard recombinant
CC   methodology. The polypeptides are useful in the treatment of disease such
CC   as diabetes, breast-, prostate-, colon cancer and other malignant tumors,
CC   hyper- and hypotension, obesity, bulimia, anorexia, growth abnormalities,
CC   asthma, manic depression, dementia, delirium, mental retardation,
CC   Huntington's disease, Tourette's syndrome, schizophrenia, growth, mental
CC   or sexual development disorders, and dysfunctions of the blood cascade
CC   system including those leading to stroke. The polynucleotides may be used
CC   as diagnostic reagents through detecting mutations in the associated gene
CC   and for chromosome localization and for tissue expression studies. The
CC   polypeptides and polynucleotides may also be used as vaccines.
XX
SQ   Sequence   753 AA;

  Query Match            54.1%;  Score 2263;  DB 22;  Length 753;
  Best Local Similarity  54.5%;  Pred. No. 8.3e-199;
  Matches  419;  Conservative  105;  Mismatches  205;  Indels   40;  Gaps   10;
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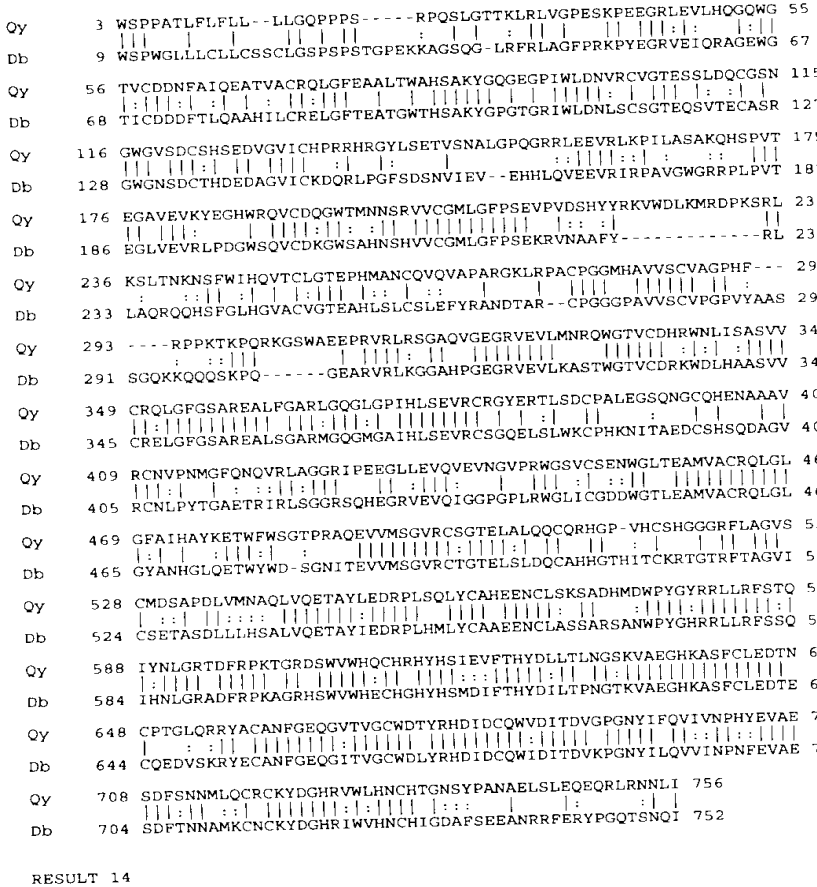

RESULT 14
AAE15549
ID AAE15549 standard; Protein; 753 AA.
XX
AC AAE15549;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human secreted protein-3 (SECP).
XX
KW Human; secreted protein; SECP-3; cell proliferative disorder; hepatitis;
KW atherosclerosis; psoriasis; autoimmune disorder; AIDS; Grave's disease;
KW acquired immunodeficiency syndrome; inflammatory disorder; osteoporosis;
KW Addison's disease; asthma; anaemia; diabetes mellitus; angina pectoris;
KW multiple sclerosis; allergy; rheumatoid arthritis; myocardial infarction;
KW cardiovascular disease; oedema; hypertension; neurological disorder;
KW gene therapy; Alzheimer's disease; Parkinson's disease; mental disorder;
KW epilepsy; renal tubular acidosis; cancer; vaccine; cataract; fungicide;
KW antibacterial; protozoacide; congenital glaucoma; transgenic animal;
KW drug screening; vulnerary; virucide; antihelminthic; antiparasitic;
KW vasotropic; nootropic; anticonvulsant; neuroleptic; tranquilliser;
KW antidepressant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..25
FT /label= Signal_peptide
FT
FT Protein 26..753
FT /label= Human_mature_SECP-3_protein
FT
FT Domain 51..145
FT /note= "Scavenger receptor cysteine-rich domain"
FT
FT Region 134..144
FT /note= "Speract receptor repeat"
FT
FT Domain 183..282
FT /note= "Scavenger receptor cysteine-rich domain"
FT
FT Domain 310..407
FT /note= "Scavenger receptor cysteine-rich domain"
FT
FT Domain 420..525
FT /note= "Scavenger receptor cysteine-rich domain"
FT
XX
PN WO200179291-A2.
XX
PD 25-OCT-2001.
XX
PF 11-APR-2001; 2001WO-US11861.
XX
PR 14-APR-2000; 2000US-197854P.
PR 04-MAY-2000; 2000US-202373P.
PR 18-MAY-2000; 2000US-205899P.
PR 01-JUN-2000; 2000US-209401P.
PR 01-JUN-2000; 2000US-210155P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Griffin JA, Yao MG, Bruns CM, Yue H, Delegeane AM, Hafalia A;
PI Patterson C, Policky JL, Tribouley CM, Baughn MR, Nguyen DB;
PI Lal P, Tang YT, Hillman JL, Lu DAM, Batra S, Au-young J, Reddy R;
PI Azimzai Y;
XX
DR WPI; 2002-066344/09.
DR N-PSDB; AAD24786.
XX
PT New human secreted proteins for treating, diagnosing or preventing cell
PT proliferative, cardiovascular, autoimmune/inflammatory, neurological
PT and developmental disorders
XX
PS Claim 1; Page 104-106; 124pp; English.
XX
CC The invention relates to an isolated human secreted protein (SECP) and
CC nucleotide molecule encoding the protein. SECP is used as vaccine. SECP
CC is used to diagnose, treat and prevent cell proliferative (e.g.
CC arteriosclerosis, atherosclerosis, hepatitis, psoriasis and cancers),
CC autoimmune/inflammatory (e.g. acquired immunodeficiency syndrome (AIDS),
CC Addison's disease, allergy, anaemia, asthma, atopic dermatitis, diabetes
CC mellitus, glomerulonephritis, trauma, multiple sclerosis, osteoporosis,
CC Grave's disease, rheumatoid arthritis, ulcerative colitis and viral,
CC bacterial, fungal, parasitic, protozoal and helminthic infections),
CC cardiovascular (e.g. angina pectoris, myocardial infarction, ischaemic
CC heart disease, hypertension, pulmonary congestion and oedema),
CC neurological (e.g. Alzheimer's disease, Huntington's disease, dementia,
CC Parkinson's disease, Creutzfeldt-Jakob disease, schizophrenia, epilepsy,
CC mental disorders including mood, anxiety and seasonal affective disorder
CC and prion diseases) and developmental disorders (e.g. renal tubular
CC acidosis, Duchenne and Becker muscular dystrophy, seizure disorders,
CC congenital glaucoma and cataract). SECP is used for creating knockin
CC humanised animals or transgenic animals to model human diseases. SECP is
CC used in somatic or germline gene therapy. SECP is used for detecting
CC differences in chromosomal location due to translocation, inversion, etc.
CC among normal, carrier or affected individuals. SECP is used as
CC hybridisation probes for mapping naturally occurring genomic sequences
CC and in a number of drug screening techniques. The present sequence is
CC human SECP-3 protein.

XX
SQ Sequence 753 AA;

Query Match 54.1%; Score 2263; DB 23; Length 753;
Best Local Similarity 54.5%; Pred. No. 8.3e-199;
Matches 419; Conservative 105; Mismatches 205; Indels 40; Gaps 10;

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Qy       3 WSPPATLFLFLL--LLGQPPPS-----RPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWG 55
Db       9 WSPWGLLLCLLCSSCLGSPSPSTGPEKKAGSQG-LRFRLAGFPRKPYEGRVEIQRAGEWG 67

Qy      56 TVCDDNFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSN 115
Db      68 TICDDDFTLQAAHILCRELGFTEATGWTHSAKYGPGTGRIWLDNLSCSGTEQSVTECASR 127

Qy     116 GWGVSDCSHSEDVGVICHPRRHRGYLSETVSNALGPQGRRLEEVRLKPILASAKQHSPVT 175
Db     128 GWGNSDCTHDEDAGVICKDQRLPGFSDSNVIEV--EHHLQVEEVRIRPAVGWGRRPLPVT 185

Qy     176 EGAVEVKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRKVWDLKMRDPKSRL 235
Db     186 EGLVEVRLPDGWSQVCDKGWSAHNSHVVCGMLGFPSEKRVNAAFY------------RL 232

Qy     236 KSLTNKNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHAVVSCVAGPHF--- 292
Db     233 LAQRQQHSFGLHGVACVGTEAHLSLCSLEFYRANDTAR--CPGGGPAVVSCVPGPVYAAS 290

Qy     293 ----RPPKTKPQRKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVV 348
Db     291 SGQKKQQQSKPQ------GEARVRLKGGAHPGEGRVEVLKASTWGTVCDRKWDLHAASVV 344

Qy     349 CRQLGFGSAREALFGARLGQGLGPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENAAAV 408
Db     345 CRELGFGSAREALSGARMGQGMGAIHLSEVRCSGQELSLWKCPHKNITAEDCSHSQDAGV 404

Qy     409 RCNVPNMGFQNQVRLAGGRIPEEGLLEVQVEVNGVPRWGSVCSENWGLTEAMVACRQLGL 468
Db     405 RCNLPYTGAETRIRLSGGRSQHEGRVEVQIGGPGPLRWGLICGDDWGTLEAMVACRQLGL 464

Qy     469 GFAIHAYKETWFWSGTPRAQEVVMSGVRCSGTELALQQCQRHGP-VHCSHGGGRFLAGVS 527
Db     465 GYANHGLQETWYWD-SGNITEVVMSGVRCTGTELSLDQCAHHGTHITCKRTGTRFTAGVI 523

Qy     528 CMDSAPDLVMNAQLVQETAYLEDRPLSQLYCAHEENCLSKSADHMDWPYGYRRLLRFSTQ 587
Db     524 CSETASDLLLHSALVQETAYIEDRPLHMLYCAAEENCLASSARSANWPYGHRRLLRFSSQ 583

Qy     588 IYNLGRTDFRPKTGRDSWVWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTN 647
Db     584 IHNLGRADFRPKAGRHSWVWHECHGHYHSMDIFTHYDILTPNGTKVAEGHKASFCLEDTE 643

Qy     648 CPTGLQRRYACANFGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAE 707
Db     644 CQEDVSKRYECANFGEQGITVGCWDLYRHDIDCQWIDITDVKPGNYILQVVINPNFEVAE 703

Qy     708 SDFSNNMLQCRCKYDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI 756
Db     704 SDFTNNAMKCNCKYDGHRIWVHNCHIGDAFSEEANRRFERYPGQTSNQI 752
```

RESULT 15
AAG66059
ID AAG66059 standard; Protein; 753 AA.
XX
AC AAG66059;
XX
DT 27-FEB-2002 (first entry)
XX
DE Human lysyl oxidase-like (LOXL3) protein.
XX
KW Lysyl oxidase; lysyl oxidase-like; LOXL; LOX; neuroprotective; nootropic;
KW dermatological; hepatotropic; cytostatic; antidote; LOXL3.
XX
OS Homo sapiens.
XX
PN WO200183702-A2.
XX
PD 08-NOV-2001.
XX
PF 03-MAY-2001; 2001WO-US14472.
XX
PR 03-MAY-2000; 2000US-201587P.
XX
PA (UYHA-) UNIV HAWAII.
XX
PI Csiszar K, Boyd CD, Kim Y, Le Saux CJ, Fong SFT;
XX
DR WPI; 2002-041491/05.
DR N-PSDB; AAI67788.
XX
PT Novel copper-dependent lysyl oxidase-like proteins, nucleic acids
PT encoding the protein for diagnostic assays and identifying modulators
PT useful for treating cancer, skin, copper-related, pulmonary or hepatic
PT disorders -
XX
PS Claim 3; Page 78; 82pp; English.
XX
CC The invention provides lysyl oxidase-like (LOXL) polypeptides and
CC polynucleotides encoding them. The LOXL proteins (LOXL3 and LOXL4) can be
CC expressed by standard recombinant methodology. The LOXL polypeptides are
CC useful for identifying their modulators which can be used for treating a
CC disorder associated with LOX or LOXL polypeptide activity, including
CC disorders related to extracellular matrix materials, a cell migration,
CC cell proliferative disorder, skin, vascular system, developmental,
CC skeletal, neurological, hepatic system, copper-related, pulmonary system
CC disorders or lathyrism disorder and cancer in a subject. The LOXL
CC polynucleotides are useful as probes and primers. The LOXL polypeptides
CC are useful in bioassays, for the production of antibodies, useful for
CC diagnostic assays to determine expression levels and localization of
CC LOXL3 and LOXL4 proteins and other proteins of the LOX gene family in
CC various tissue samples from healthy or infirm subjects and to purify the
CC proteins. The antibodies are therapeutically useful to counteract or
CC supplement the biological effect of LOXL proteins in vivo. The present
CC sequence represents a human-derived LOXL3 protein.
XX
SQ Sequence 753 AA;

Query Match 54.1%; Score 2263; DB 23; Length 753;
Best Local Similarity 54.5%; Pred. No. 8.3e-199;
Matches 419; Conservative 105; Mismatches 205; Indels 40; Gaps 10;

```
Qy       3 WSPPATLFLFLL--LLGQPPPS-----RPQSLGTTKLRLVGPESKPEEGRLEVLHQGQWG 55
Db       9 WSPWGLLLCLLCSSCLGSPSPSTGPEKKAGSQG-LRFRLAGFPRKPYEGRVEIQRAGEWG 67

Qy      56 TVCDDNFAIQEATVACRQLGFEAALTWAHSAKYGQGEGPIWLDNVRCVGTESSLDQCGSN 115
Db      68 TICDDDFTLQAAHILCRELGFTEATGWTHSAKYGPGTGRIWLDNLSCSGTEQSVTECASR 127

Qy     116 GWGVSDCSHSEDVGVICHPRRHRGYLSETVSNALGPQGRRLEEVRLKPILASAKQHSPVT 175
Db     128 GWGNSDCTHDEDAGVICKDQRLPGFSDSNVIEV--EHHLQVEEVRIRPAVGWGRRPLPVT 185

Qy     176 EGAVEVKYEGHWRQVCDQGWTMNNSRVVCGMLGFPSEVPVDSHYYRKVWDLKMRDPKSRL 235
Db     186 EGLVEVRLPDGWSQVCDKGWSAHNSHVVCGMLGFPSEKRVNAAFY------------RL 232

Qy     236 KSLTNKNSFWIHQVTCLGTEPHMANCQVQVAPARGKLRPACPGGMHAVVSCVAGPHF--- 292
Db     233 LAQRQQHSFGLHGVACVGTEAHLSLCSLEFYRANDTAR--CPGGGPAVVSCVPGPVYAAS 290

Qy     293 ----RPPKTKPQRKGSWAEEPRVRLRSGAQVGEGRVEVLMNRQWGTVCDHRWNLISASVV 348
Db     291 SGQKKQQQSKPQ------GEARVRLKGGAHPGEGRVEVLKASTWGTVCDRKWDLHAASVV 344

Qy     349 CRQLGFGSAREALFGARLGQGLGPIHLSEVRCRGYERTLSDCPALEGSQNGCQHENAAAV 408
```

```
                ||:|||||||||||| |||:|||:| |||||||| | | :|  ||     :   | |   | |
Db     345 CRELGPGSAREALSGARMGQGMGAIHLSEVRCSGQELSLWKCPHKNITAEDCSHSQDAGV 404

Qy     409 RCNVPNMGFQNQVRLAGGRIPEEGLLEVQVEVNGVPRWGSVCSENWGLTEAMVACRQLGL 468
           |||:|  | : ::|||:|||   || :|||:   |  ||| :| ::|| ||||||||||
Db     405 RCNLPYTGAETRIRLSGGRSQHEGRVEVQIGGPGPLRWGLICGDDWGTLEAMVACRQLGL 464

Qy     469 GFAIHAYKETWFWSGTPRAQEVVMSGVRCSGTELALQQCQRHGP-VHCSHGGGRFLAGVS 527
           |:| |  :|||:|  :    |||||||||:||||:| ||  ||  : |   | || |||
Db     465 GYANHGLQETWYWD-SGNITEVVMSGVRCTGTELSLDQCAHHGTHITCKRTGTRFTAGVI 523

Qy     528 CMDSAPDLVMNAQLVQETAYLEDRPLSQLYCAHEENCLSKSADHMDWPYGYRRLLRFSTQ 587
           | ::| ||:::: |||||||:|||||  |||| |||||: ||   :||||:|||||||:|
Db     524 CSETASDLLLHSALVQETAYIEDRPLHMLYCAAEENCLASSARSANWPYGHRRLLRFSSQ 583

Qy     588 IYNLGRTDFRPKTGRDSWVWHQCHRHYHSIEVFTHYDLLTLNGSKVAEGHKASFCLEDTN 647
           |:|||| ||||| || |||||:|| ||||:::|||||:|| ||:|||||||||||||||
Db     584 IHNLGRADFRPKAGRHSWVWHECHGHYHSMDIFTHYDILTPNGTKVAEGHKASFCLEDTE 643

Qy     648 CPTGLQRRYACANFGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAE 707
           |   : :|| ||||||||:|||||| |||||||||:|||||  ||||| ||::||::||||
Db     644 CQEDVSKRYECANFGEQGITVGCWDLYRHDIDCQWIDITDVKPGNYILQVVINPNFEVAE 703

Qy     708 SDFSNNMLQCRCKYDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI 756
           |||:|| ::| |||||||:|:|||| |:::   |    |:     :| |
Db     704 SDFTNNAMKCNCKYDGHRIWVHNCHIGDAFSEEANRRFERYPGQTSNQI 752
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